



Zeren Gao et al.  
Serial No. 09/706,968

#### Appendix

Please replace the paragraph at page 11, lines 7-12 with the following amended paragraph:

[Fig. 1 is] Figs. 1A-1G are a Hopp/Woods hydrophilicity profile of the amino acid sequence shown in SEQ ID NO:2. The profile is based on a sliding six-residue window. Buried G, S, and T residues and exposed H, Y, and W residues were ignored. These residues are indicated in the [figure] figures by lower case letters.

— Please replace the paragraph at page 30, line 22 through page 31, line 3 with the following amended paragraph:

Amino acid sequence changes are made in zveg3 polypeptides so as to minimize disruption of higher order structure essential to biological activity. In general, conservative amino acid changes are preferred. Changes in amino acid residues will be made so as not to disrupt the cystine knot and "bow tie" arrangement of loops in the growth factor domain that is characteristic of the protein family. Conserved motifs will also be maintained. The effects of amino acid sequence changes can be predicted by computer modeling as disclosed above or determined by analysis of crystal structure (see, e.g., Laphorn et al., *ibid.*). A hydrophobicity profile of SEQ ID NO:2 is shown in [Fig. 1] Figs. 1A-1G. Those skilled in the art will recognize that this hydrophobicity will be taken into account when designing alterations in the amino acid sequence of a zveg3 polypeptide, so as not to disrupt the overall profile. Additional guidance in selecting amino acid substitutions is provided by the alignment of mouse and human zveg3 sequences shown in Fig. 6.

#### In the Claims:

Please replace claims 46 and 53 with the following amended claims:

46. (amended) A method for promoting the proliferation of fibroblasts or smooth muscle cells in a mammal comprising administering to said mammal a composition comprising:

a protein comprising a first polypeptide disulfide bonded to a second polypeptide, wherein each of said first and second polypeptides is from 111 to 136 amino acid residues in length and comprises residues 235-345 of SEQ ID NO:2; and

a pharmaceutically acceptable vehicle,

in an amount [to] sufficient to increase cell proliferation.